



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Tripp, Cynthia A.
Frank, Glenn R.
Grieve, Robert B.

(ii) TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
P22U PROTEINS

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/460,428
(B) FILING DATE: 02-JUN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Connell, Gary J.
(B) REGISTRATION NUMBER: 32,020
(C) REFERENCE/DOCKET NUMBER: 2618-13-3

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 913 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GC GAG TTA AAT AGT CGA ATT TCC GGA GTA CAC CGT AAT ACT GCA GGT

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Glu	Leu	Asn	Ser	Arg	Ile	Ser	Gly	Val	His	Arg	Asn	Thr	Ala	Gly		
1		5			10				15							
GCT	TTA	CAA	CGA	TTT	GCT	CTA	AAT	GGT	CAA	AAT	ACT	CTT	AAC	GAA	GGA	95
Ala	Leu	Gln	Arg	Phe	Ala	Leu	Asn	Gly	Gln	Asn	Thr	Leu	Asn	Glu	Gly	
		20						25					30			
TCA	AGT	TAT	GAG	CCA	AAC	GGA	CTA	TTT	GTA	TTT	TCA	GCA	ATA	AAC	GGT	143
Ser	Ser	Tyr	Glu	Pro	Asn	Gly	Leu	Phe	Val	Phe	Ser	Ala	Ile	Asn	Gly	
		35						40				45				
AGC	CAT	ACT	GAT	AGC	TTA	TCT	CAG	TAT	GGT	GAA	GGA	ATA	AAT	GAA	AAT	191
Ser	His	Thr	Asp	Ser	Leu	Ser	Gln	Tyr	Gly	Glu	Gly	Ile	Asn	Glu	Asn	
	50					55				60						
TAT	CAT	TCT	GGA	ACT	AAT	TAT	TAT	GAT	GAA	GTA	GAA	TTA	AGA	GAT	AAA	239
Tyr	His	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Glu	Val	Glu	Leu	Arg	Asp	Lys	
	65				70				75							
ACA	AAT	CAG	ACA	TCG	TAC	ATT	AAT	GGA	AAT	GAT	AAT	GGA	ATC	AAT	GGA	287
Thr	Asn	Gln	Thr	Ser	Tyr	Ile	Asn	Gly	Asn	Asp	Asn	Gly	Ile	Asn	Gly	
	80					85			90			95				
AAG	GAT	GAT	GAA	GAT	CTG	GAT	GAA	TGC	TCT	GAT	CAA	GAA	TTC	CGA	TGT	335
Lys	Asp	Asp	Glu	Asp	Leu	Asp	Glu	Cys	Ser	Asp	Gln	Glu	Phe	Arg	Cys	
	100					105				110						
CCA	TAT	CTA	GCT	AAA	ACA	CTT	TGT	GTT	CAT	TAT	TTG	AAA	ATA	TGC	GAT	383
Pro	Tyr	Leu	Ala	Lys	Thr	Leu	Cys	Val	His	Tyr	Leu	Lys	Ile	Cys	Asp	
	115					120				125						
GGT	ATT	GAT	GAT	TGT	GGT	GAT	GGA	AGT	GAT	GAA	ATG	AAC	TGT	GCT	GAT	431
Gly	Ile	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Met	Asn	Cys	Ala	Asp	
	130					135				140						
GAT	GAA	GTG	ATA	ACA	TCA	ATA	AAT	GGT	AAC	GAA	TCA	ATC	AAT	ATC	AGA	479
Asp	Glu	Val	Ile	Thr	Ser	Ile	Asn	Gly	Asn	Glu	Ser	Ile	Asn	Ile	Arg	
	145					150				155						
TGT	GAT	CCG	GAT	CAA	TTT	CGA	TGT	GAA	AAT	GGA	AAA	TGT	ATC	GCA	CAA	527
Cys	Asp	Pro	Asp	Gln	Phe	Arg	Cys	Glu	Asn	Gly	Lys	Cys	Ile	Ala	Gln	
	160					165			170			175				
ATT	GAT	CGA	TGT	AAT	CGA	AAA	TAT	GAT	TGT	GAT	GAT	GGT	ACA	GAT	GAA	575
Ile	Asp	Arg	Cys	Asn	Arg	Lys	Tyr	Asp	Cys	Asp	Asp	Gly	Thr	Asp	Glu	
	180					185				190						
ACA	ACT	TGT	GAA	TAT	TTC	GTG	CAA	GCT	TTG	CAA	CAA	GCG	AGA	GGT	GTA	623
Thr	Thr	Cys	Glu	Tyr	Phe	Val	Gln	Ala	Leu	Gln	Gln	Ala	Arg	Gly	Val	
	195					200				205						
ACG	GTG	CAG	GAT	AAT	GCA	ATT	CGA	GAT	GAC	GAG	ATA	CCA	AAT	TAT	ACT	671
Thr	Val	Gln	Asp	Asn	Ala	Ile	Arg	Asp	Asp	Glu	Ile	Pro	Asn	Tyr	Thr	
	210					215				220						
GTA	TCC	ATG	GAA	CAG	AAA	TAC	GAT	CAA	GTA	AAG	GAA	GAT	AAG	GAG	CGG	719
Val	Ser	Met	Glu	Gln	Lys	Tyr	Asp	Gln	Val	Lys	Glu	Asp	Lys	Glu	Arg	
	225					230				235						
CGA	ATG	CAA	GAG	GAG	GAG	GAA	CAG	GAA	AGG	CTG	AGA	GAG	TAC	GAG	GAA	767
Arg	Met	Gln	Glu	Glu	Glu	Gln	Glu	Glu	Arg	Leu	Arg	Glu	Tyr	Glu	Glu	

240	245	250	255	
CAG ATA CAG GAA AAA TTG AGG CAG GAG GAA GAA AGA GAA CGG CAA GAA Gln Ile Gln Glu Lys Leu Arg Gln Glu Glu Glu Arg Glu Arg Gln Glu 260 265 270				815
CAG GAA AGA AGA CAA AAG GAA CGA GAA AGA ATG GAA CAA GAA AGG ATA Gln Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile 275 280 285				863
AGA CAA GAA TAT GAT GAA AAG GAA AGA CAA AGG CAA TAT GCT GAA CAG Arg Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln 290 295 300				911
GC				913

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu	Leu	Asn	Ser	Arg	Ile	Ser	Gly	Val	His	Arg	Asn	Thr	Ala	Gly	Ala
1					5				10						15
Leu Gln Arg Phe Ala Leu Asn Gly Gln Asn Thr Leu Asn Glu Gly Ser															
					20			25							30
Ser Tyr Glu Pro Asn Gly Leu Phe Val Phe Ser Ala Ile Asn Gly Ser															
					35			40							45
His Thr Asp Ser Leu Ser Gln Tyr Gly Glu Gly Ile Asn Glu Asn Tyr															
					50			55							60
His Ser Gly Thr Asn Tyr Tyr Asp Glu Val Glu Leu Arg Asp Lys Thr															
					65			70							80
Asn Gln Thr Ser Tyr Ile Asn Gly Asn Asp Asn Gly Ile Asn Gly Lys															
					85			90							95
Asp Asp Glu Asp Leu Asp Glu Cys Ser Asp Gln Glu Phe Arg Cys Pro															
					100			105							110
Tyr Leu Ala Lys Thr Leu Cys Val His Tyr Leu Lys Ile Cys Asp Gly															
					115			120							125
Ile Asp Asp Cys Gly Asp Gly Ser Asp Glu Met Asn Cys Ala Asp Asp															
					130			135							140
Glu Val Ile Thr Ser Ile Asn Gly Asn Glu Ser Ile Asn Ile Arg Cys															
					145			150							160
Asp Pro Asp Gln Phe Arg Cys Glu Asn Gly Lys Cys Ile Ala Gln Ile															
					165			170							175

Asp Arg Cys Asn Arg Lys Tyr Asp Cys Asp Asp Gly Thr Asp Glu Thr
 180 185 190
 Thr Cys Glu Tyr Phe Val Gln Ala Leu Gln Gln Ala Arg Gly Val Thr
 195 200 205
 Val Gln Asp Asn Ala Ile Arg Asp Asp Glu Ile Pro Asn Tyr Thr Val
 210 215 220
 Ser Met Glu Gln Lys Tyr Asp Gln Val Lys Glu Asp Lys Glu Arg Arg
 225 230 235 240
 Met Gln Glu Glu Glu Glu Gln Glu Arg Leu Arg Glu Tyr Glu Glu Gln
 245 250 255
 Ile Gln Glu Lys Leu Arg Gln Glu Glu Arg Glu Arg Gln Glu Gln
 260 265 270
 Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile Arg
 275 280 285
 Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln
 290 295 300

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..626

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 627..1016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GT TTT GTT GTA CTA CTC GTT GCA ATA TGG ATT GAA ATG AGC CAA	47
Phe Val Val Leu Leu Val Val Ala Ile Trp Ile Glu Met Ser Gln	
1 5 10 15	
GGC CAA CAA ATG ATC AAA CAA TGT AAA TGT TCT GAT ATT GCA CCA TGT	95
Gly Gln Gln Met Ile Lys Gln Cys Lys Cys Ser Asp Ile Ala Pro Cys	
20 25 30	
CAA TTA ACT GCC GTT CAA TCA GTT TTA CCA TGT GCT GAT CAA TGC CAG	143
Gln Leu Thr Ala Val Gln Ser Val Leu Pro Cys Ala Asp Gln Cys Gln	
35 40 45	
AAA TAT ATT ACT TCA ATT GGT GGT AAT TAT GAT CAA ATT AGT AAC TGT	191
Lys Tyr Ile Thr Ser Ile Gly Gly Asn Tyr Asp Gln Ile Ser Asn Cys	
50 55 60	

TTT AAA CAG AAA CAA TCA ATT ATA AAT GAT GCT ATG AAA TGT GCT CAA Phe Lys Gln Lys Gln Ser Ile Ile Asn Asp Ala Met Lys Cys Ala Gln 65 70 75	239
GAT GCT TTC CCA AAT GCA TGC GCA CAA GGT GAA CCA AAA ATG GTA CCA Asp Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys Met Val Pro 80 85 90 95	287
AAA CGA TTC GGA AAA GGT CTT CAA TTA GCT GTA ATG ACT GAT ATC AAC Lys Arg Phe Gly Lys Gly Leu Gln Leu Ala Val Met Thr Asp Ile Asn 100 105 110	335
AAA GAA TTA CAA CGA ATG GGA ATA GCA AAT CAA GTT ACT CAA CTA ATC Lys Glu Leu Gln Arg Met Gly Ile Ala Asn Gln Val Thr Gln Leu Ile 115 120 125	383
TCC CAA GGT CGA CGA TTC TTT AAA TGC TTC CAA TCG TGT ATG ATG AAA Ser Gln Gly Arg Arg Phe Phe Lys Cys Phe Gln Ser Cys Met Met Lys 130 135 140	431
AAA TTG GGC TCA TGT TCT CCA GAT TGT GGT CTT GAT TTA CCA TCT GAT Lys Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp 145 150 155	479
AAT GTT ATG GTT CAA ACA GTT AAA AAT TGC GCT CAA AAA AGT GGT ATT Asn Val Met Val Gln Thr Val Lys Asn Cys Ala Gln Lys Ser Gly Ile 160 165 170 175	527
CAA ACT GCA TCG GTG CAA GAT CTT TGC TTT TGC GTC GAA CAA GCT GGT Gln Thr Ala Ser Val Gln Asp Leu Cys Phe Cys Val Glu Gln Ala Gly 180 185 190	575
ATT CGG CAA CTT TCT GAT GTA TGT CCT CGT ATA CAA ATT TTC AAA ACG Ile Arg Gln Leu Ser Asp Val Cys Pro Arg Ile Gln Ile Phe Lys Thr 195 200 205	623
AAA TGAGTATTGA GAATATTGCA CTAGCAGCAA TCATTATTT TCTCGAGAAT Lys	676
TTTCGCTATC AATAAGTTGG AATATGATTA CAATAATATA TATATTAAC T GCAAAATCT	736
TTCTTCTTCA AAATTATTTT TCATTTGCT CTCATAATTG CATGATAATA GTCATAATGA	796
AAAACAGGTT TTCTTTTTT AAAATGATAA CTTCAAACAA ATAGGTATTT CTTGATATAT	856
ATATGTATGT ATGTATGTGT GTGTGTGTGT GTGTGTGTAT GTGTGTGTT GTGTATGTGT	916
ATATGTATGT ATGTATGTAT GTATGTATGT ATGTGTAGGA GAAAAGCAAA CTAACAGTA	976
AATGAAAGAA AAAATAAGT CAAATAAAAG TTTGATAATT	1016

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe Val Val Leu Leu Val Val Ala Ile Trp Ile Glu Met Ser Gln Gly
1 5 10 15

Gln Gln Met Ile Lys Gln Cys Lys Cys Ser Asp Ile Ala Pro Cys Gln
20 25 30

Leu Thr Ala Val Gln Ser Val Leu Pro Cys Ala Asp Gln Cys Gln Lys
35 40 45

Tyr Ile Thr Ser Ile Gly Gly Asn Tyr Asp Gln Ile Ser Asn Cys Phe
50 55 60

Lys Gln Lys Gln Ser Ile Ile Asn Asp Ala Met Lys Cys Ala Gln Asp
65 70 75 80

Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys Met Val Pro Lys
85 90 95

Arg Phe Gly Lys Gly Leu Gln Leu Ala Val Met Thr Asp Ile Asn Lys
100 105 110

Glu Leu Gln Arg Met Gly Ile Ala Asn Gln Val Thr Gln Leu Ile Ser
115 120 125

Gln Gly Arg Arg Phe Phe Lys Cys Phe Gln Ser Cys Met Met Lys Lys
130 135 140

Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp Asn
145 150 155 160

Val Met Val Gln Thr Val Lys Asn Cys Ala Gln Lys Ser Gly Ile Gln
165 170 175

Thr Ala Ser Val Gln Asp Leu Cys Phe Cys Val Glu Gln Ala Gly Ile
180 185 190

Arg Gln Leu Ser Asp Val Cys Pro Arg Ile Gln Ile Phe Lys Thr Lys
195 200 205

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Asp Cys Gly Asp Gly Ser Asp Glu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Gln Asp Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Ile Ala Pro Cys Gln Leu Thr Ala Val Gln Ser Val Leu Pro Cys
1 5 10 15

Ala Asp Gln Cys Gln Lys
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp Asn
1 5 10 15

Val Met Val Gln Asp Val
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGATCCCG AGTTAAATAG TCG

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCAGGATCC TGCACCG

17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGAGAGAGA GAGAGAGAGA ACTAGTCTCG AGTTTTTTT TTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGYTCNCCNG AYTGYGG

17

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGYAGTCCNG AYTGYGG

17

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /label= PROBE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGNACCATNA CRTTRTC

17

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /label= PROBE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGTTTGAAC CATAACATTA CAGATGG

27

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..25
(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTGCAATAT GGGATCCAAT GAGCC

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..25
(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCTAGTGCA GGATCCTCAA TACTC

25